SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding them for the Treatment or Prevention of Diseases
<130> 032723woJH
<140>
<141>
<160> 12
<170> PatentIn Ver. 2.1

<210> 1
<211> 618
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(615)

<400> 1
atg tcg cgc ggc ctc cag ctt ctg ctc ctg agc tgc gcc tac agc ctg 48
Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
1 5 10 15

gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac 96
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
20 25 30

ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc 144
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
35 40 45

tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag 192
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
50 55 60

gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt 240
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
65 70 75 80

tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac 288
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
85 90 95

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg 336
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
100 105 110

gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga 384
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
115 120 125

tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag 432
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
130 135 140

att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att 480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145 150 155 160

ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct 528

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Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
                165                 170                 175

aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag   576
Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
            180                 185                 190

cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga           618
His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
        195                 200                 205
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<210> 2
<211> 205
<212> PRT
<213> Homo sapiens

<400> 2

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Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
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Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
            20                  25                  30

Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
        35                  40                  45

Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
    50                  55                  60

Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
65                  70                  75                  80

Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
                85                  90                  95

Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
            100                 105                 110

Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
        115                 120                 125

Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
    130                 135                 140

Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145                 150                 155                 160

Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
                165                 170                 175

Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
            180                 185                 190

His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
        195                 200                 205
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<210> 3
<211> 2051
<212> DNA
<213> Mus musculus
<220>

<221> CDS
<222> (14)..(601)

<400> 3

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gcgctccagc cgc atg tcg caa ggc ctc cag ctc ctg ttt cta ggc tgc    49
                Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys
                  1               5                  10

gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct    97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
         15                  20                  25

tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag   145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
     30                  35                  40

ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag   193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu
 45                  50                  55                  60

agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc   241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro
                 65                  70                  75

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc   289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser
             80                  85                  90

tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac   337
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn
         95                  100                 105

ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct   385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala
    110                 115                 120

aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc   433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe
125                 130                 135                 140

tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt   481
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe
                145                 150                 155

gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa   529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu
            160                 165                 170

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg   577
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val
        175                 180                 185

acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggt ttttacaaag  631
Thr Leu Pro Lys Thr Glu Thr Val
    190                 195

ccaagggcac atcagatcag tgtgcctgaa tgccacccgg acaagagaag aatgagctcc 691

atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc 751

cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct 811
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ctgtggctgt cagcttaatg tttcatgtgg ctatctggtc aacctcgtga gtgcttttca 871

gtcatctaca agctatggtg agatgcaggt gaagcagggt catgggaaat ttgaacactc 931

tgagctggcc ctgtgacaga ctcctgagga cagctgtcct ctcctacatc tgggatacat 991

ctctttgaat ttgtcctgtt tcgttgcacc agcccagatg tctcacatct ggcggaaatt 1051

gacaggccaa gctgtgagcc agtgggaaat atttagcaaa taatttccca gtgcgaaggt 1111

cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc 1171

cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca 1231

catttatttt tttaatcttc atgtacttgt caaagaagaa tttttcatgt tttttcaaag 1291

aagtgtgttt ctttcctttt ttaaaatatg aaggtctagt tacatagcat tgctagctga 1351

caagcagcct gagagaagat ggagaatgtt cctcaaaata gggacagcaa gctagaagca 1411

ctgtacagtg ccctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac 1471

aagattgtct gtatgattct ggacgagtca cttgtggttt tcactctctg gttagtaaac 1531

cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg 1591

tagtgaatac attggcaact ctactgggct gttaccttgt tgatatccta gagttctgga 1651

gctgagcgaa tgcctgtcat atctcagctt gcccatcaat ccaaacacag gaggctacaa 1711

aaaggacatg agcatggtct tctgtgtgaa ctcctcctga gaaacgtgga gactggctca 1771

gcgctttgcg cttgaaggac taatcacaag ttcttgaaga tatggaccta ggggagctat 1831

tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatttctt 1891

taatgagctg ggctccttcc tcatttgctt cccaaagaga ttttgtccca ctaatggtgt 1951

gcccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc 2011

tcagccatga ctttcatgct attaaaagaa tgcatgtgaa 2051

<210> 4
<211> 196
<212> PRT
<213> Mus musculus

<400> 4

Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys Ala Cys Ser Leu
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Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala Cys Ser Glu Thr
20 25 30

Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
35 40 45

Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
50 55 60

Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala

65 70 75 80

Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
85 90 95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
100 105 110

Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
115 120 125

Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
130 135 140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
145 150 155 160

Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
165 170 175

Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
180 185 190

Thr Glu Thr Val
195

<210> 5
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer for CD83ext

<400> 5
tcccccggga acgccggagg tgaaggtggc t 31

<210> 6
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer for CD83ext

<400> 6
aattagaatt ctcaaatctc cgctctgtat t 31

<210> 7
<211> 435
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext
<220>
<221> CDS
<222> (1)..(417)
<220>
<221> mat_peptide
<222> (28)..(417)

<400> 7
cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag 48
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
-5 -1 1 5

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
10 15 20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
25 30 35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
90 95 100

agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa 384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
105 110 115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120 125 130

<210> 8
<211> 139
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: partial sequence of pGEX2ThCD83ext

<400> 8
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
-5 -1 1 5

Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
10 15 20

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
25 30 35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85

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Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
        90                  95                 100

Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
    105                 110                 115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120                 125                 130
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<210> 9
<211> 435
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: partial sequence of pGEX2ThCD83ext_mut129_CtoS
<220>
<221> CDS
<222> (1)..(417)
<220>
<221> mat_peptide
<222> (28)..(417)

<400> 9

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cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag   48
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
                -5                  -1   1                   5

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc   96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
         10                  15                  20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag   144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
     25                  30                  35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga   192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40                  45                  50                  55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat   240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
                60                  65                  70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg   288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
            75                  80                  85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta   336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
        90                  95                 100

agt ggc aag gtg atc ttg aga gtg aca gga tcc cct gca cag cgt aaa   384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
    105                 110                 115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact   435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120                 125                 130
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<210> 10
<211> 139
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: partial sequence of pGEX2ThCD83ext_mut129_CtoS

<400> 10

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Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
                -5                  -1   1                   5

Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
        10                  15                  20

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
    25                  30                  35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40                  45                  50                  55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
                60                  65                  70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
            75                  80                  85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
        90                  95                  100

Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
    105                 110                 115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120                 125                 130
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<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer sense-pGEX2ThCD83

<400> 11
tccccccggg aacgccggag gtgaaggtgg ct 32

<210> 12
<211> 66
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer antisense-CD83extra_mutantCtoS

<400> 12
aattagaatt ctcaaatctc cgctctgtat ttcttaaaag tctcttcttt acgctgtgca 60
ggggat 66

<210> 13

<211> 209
<212> PRT
<213> Homo sapiens

<400> 13

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Gly Ser Pro Gly Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys
1               5                  10                  15

Ala Tyr Ser Leu Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser
            20                  25                  30

Glu Asp Val Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro
        35                  40                  45

Tyr Thr Val Ser Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met
    50                  55                  60

Glu Thr Pro Gln Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys
65                  70                  75                  80

Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu
                85                  90                  95

Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr
            100                 105                 110

Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu
        115                 120                 125

Arg Val Thr Gly Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys
    130                 135                 140

Arg Arg Ala Glu Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu
145                 150                 155                 160

Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe
                165                 170                 175

Pro Asp Phe Ser Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr
            180                 185                 190

Ser Pro Asn Lys His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu
        195                 200                 205

Val
209
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